

the claims pages accordingly.

### **IN THE CLAIMS**

Please substitute the following amended claims for corresponding claims previously presented. A copy of the amended claims showing current revisions is attached.

1. (Amended) A method for determining an amino acid sequence motif or a pentidomimetic sequence motif containing an active site capable of being bound by an enzyme which catalyses covalent modification of a substrate molecule, comprising;

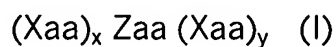
a) contacting the enzyme with a library consisting of a number of oriented degenerate library subsets of molecules, each subset comprising unmodified degenerate motif sequences each having n residues and each having a modifiable residue at a different fixed non-degenerate position, under conditions which allow for modification of molecules which are a substrate for the enzyme;

b) allowing the enzyme to modify modifiable residues in library subsets containing molecules having an active substrate site for the enzyme;

c) deconvoluting the oriented degenerate library subsets of the library, *in situ* without separating modified from unmodified molecules, so as to reveal the

sequence of any motif which has been modified by covalent binding of the enzyme;

wherein each library subset is of formula (I)



wherein

Zaa is a non-degenerate modifiable natural or unnatural amino acid residue or peptidomimetic;

Xaa is any natural or unnatural amino acid residue or peptidomimetic;

x and y are each independently 0 or an integer;

$(x + y) = n-1$ ; and

n = an integer from 3 to 8, preferably 5.